TITLE: METHOD AND APPARATUS FOR
AUTOMATICALLY ...
INVENTORS: Kensaku Imai et al.
SERIAL NO.: 09/785,269
DOCKET NO.: 826.1335C
Replacement Sheet filed 12/31/03

FIG. 3

DNA FRAGMENT LABELED WITH ^{32}P AT 5' EDGE

SEQ ID: 7

^{32}Ⓟ—TGCACTTGAACGCATGCT

RADIOACTIVE FRAGMENTS OF VARIOUS LENGTHS THROUGH CHEMICAL PROCESS OF SPECIFIC CLEAVING WITH RESIDUAL BASE A

SEQ ID: 8

^{32}Ⓟ—TGCACTTGAACGC   TGCT

SEQ ID: 9

^{32}Ⓟ—TGCACTTGA   CGCATGCT

SEQ ID: 9

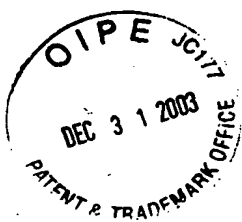^{32}Ⓟ—TGCACTTG   ACGCATGCT

SEQ ID: 10

^{32}Ⓟ—TGC   CTTGAACGCATGCT
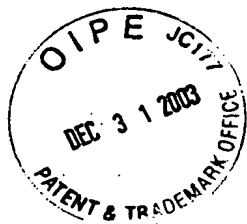
RADIOACTIVE
FRAGMENT

UNLABELED
FRAGMENT

THESE FRAGMENTS CAN BE STRICTLY ISOLATED DEPENDING ON LENGTH THROUGH GEL ELECTROPHORESIS

ELECTROPHORESIS

GEL

FIG. 4

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VECTOR DB FORMAT

```
>ID
PUC18
>SEQ ID: 11
TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGAT
GCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAGA
GCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC
ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGG
GGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGCCAA
GCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCGGGTACCGAGCTCGAATTCGTAATCATGGTCATAGCTGTTTCCT
GTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATG
AGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAAT
GAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG
GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGG
AAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCC
GCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG
TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTC
GGGAAGCGTGGCGCTTTCTCAAAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTG
TGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC
TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTG
GTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAG
TTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGA
AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGAT
TTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTA
TATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCA
TCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGAT
ACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTC
CTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTG
CGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCA
ACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAA
GTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGC
TTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTC
AATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCT
CAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTC
ACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAAT
ACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTA
TTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATC
ATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTC
>MULTI
399..450
```

FIG. 9

(* INDICATES MULTIPLE CLONING SITE)

****

SEQ ID: 12   GTGCCAAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCGGGTACCGAGCTCGAATTCGTAAT

SEQ ID: 13   AAGCTT→HIND III

SEQ ID: 14   GCATGC→SPH I

SEQ ID: 15   CTGCAG→PST I

SEQ ID: 16   GTCGAC→SAL I, ACC I, HINC II

SEQ ID: 17   TCTAGA→XBA I

SEQ ID: 18   GGATCC→BAMH I

SEQ ID: 19   CCCGGG →SMA I, XMA I

SEQ ID: 20   GGTACC →KPN I

SEQ ID: 21   GAGCTC →SAC I

SEQ ID: 22   GAATTC →ECOR I

FIG. 10

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WHEN HIND Ⅲ IS SPECIFIED ON VECTOR 5' SIDE
XBA I IS SPECIFIED ON VECTOR 3' SIDE, HIND Ⅲ IS
SPECIFIED ON OBJECT DNA 5' SIDE, AND XBA I IS
SPECIFIED ON OBJECT DNA 3' SIDE

(✱✱✱✱ INDICATES RESIDUAL MULTIPLECLONING SITE
(┼┼┼┼┼ INDICATES AN OBJECT DNA FRAGMENT

(SEQ ID NO. 4)   (SEQ ID NO. 23)
      ✱✱✱✱✱   ✱✱✱✱✱✱✱✱✱✱✱✱✱✱✱✱✱✱✱✱✱✱✱✱✱✱✱✱✱
GTGCCAAGCTT┼┼┼┼┼┼┼┼┼┼┼┼┼┼┼┼┼┼┼┼TCTAGAGGATCCCCGGGTACCGAGCTCGAATTCGTAAT
      AAGCTT   TCTAGA
         ⇧   ⇧
5' SIDE RETRIEVAL KEY   9' SIDE RETRIEVAL KEY
(IN THIS EXAMPLE,   (IN THIS EXAMPLE, XBA I SITE)
HIND Ⅲ SITE)

FIG. 17